

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,
- (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 30-AUG-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Wetherell, Jr. Ph.D., John W.
 - (B) REGISTRATION NUMBER: 31,678
 - (C) REFERENCE/DOCKET NUMBER: PD-1294
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-455-5100
 - (B) TELEFAX: 619-455-5110

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2075 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: DB60R32
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 130..1177
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG

CCAGCGCTCC AGGCCCCGCG CTCCTCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA	120
GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC	168
Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe	
1 5 10	
GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC	216
Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys	
15 20 25	
AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCC CCG CGC TGC CCG GCC	264
Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala	
30 35 40 45	
GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC	312
Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala	
50 55 60	
AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC	360
Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His	
65 70 75	
AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC	408
Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly	
80 85 90	
GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG	456
Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val	
95 100 105	
TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG	504
Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr	
110 115 120 125	
TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT	552
Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val	
130 135 140	
CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC	600
Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro	
145 150 155	
GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648
Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr	
160 165 170	
GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696
Val Val Gly Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly	
175 180 185	
CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744
Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu	
190 195 200 205	
TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792
Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val	
210 215 220	
ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840
Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys	
225 230 235	
ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888
Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly	

240	245	250	
AAA AAG TGC ATC CGT ACT CCC Lys Lys Cys Ile Arg Thr Pro 255 260	AAA ATC TCC AAG CCT ATC AAG TTT GAG Lys Ile Ser Lys Pro Ile Lys Phe Glu 265		936
CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly 270 275 280 285			984
GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu 290 295 300			1032
CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met 305 310 315			1080
ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn 320 325 330			1128
GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala 335 340 345			1177
GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACTGA TTCACATCTC			1237
ATTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG			1297
GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC			1357
CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC			1417
CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT			1477
CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA			1537
AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC			1597
CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA			1657
CATTCTGATT CGAATGACAC TGTTCAAGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT			1717
TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAATATT			1777
GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA			1837
AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA			1897
TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT			1957
ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA			2017
GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG			2075

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu
1				5					10					15	
Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
			20					25					30		
Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
		35					40					45			
Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
	50					55					60				
Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
65					70					75					80
Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr
				85					90					95	
Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser
			100					105					110		
Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
		115					120					125			
Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro
	130					135					140				
Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys
145					150					155					160
Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly
				165					170					175	
Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro
			180					185					190		
Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala
		195					200					205			
Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp
	210					215					220				
Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg
225					230					235					240
Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys
				245					250					255	
Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly
			260					265					270		
Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr
		275					280					285			
Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu
	290					295						300			
Phe	Lys	Cys	Pro	Asp	Gly	Glu	Val	Met	Lys	Lys	Asn	Met	Met	Phe	Ile
305					310					315					320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
340 345